

Untitled  
GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; Search time 974.359  
Seconds

(without alignments)  
944.877 Million cell

updates/sec

Title: US-10-623-880-1  
Perfect score: 19  
Sequence: 1 tccgtaggtgaacctgcgg 19

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	19	6	AR036914	AR036914 Sequence
2	19	100.0	19	6	AR043154	AR043154 Sequence
3	19	100.0	19	6	AR050515	AR050515 Sequence
4	19	100.0	19	6	AR074654	AR074654 Sequence
5	19	100.0	19	6	AR097249	AR097249 Sequence
6	19	100.0	19	6	AR147481	AR147481 Sequence

# Untitled

	7	19	100.0	19	6	AR153773	AR153773 Sequence
	8	19	100.0	19	6	AR178320	AR178320 Sequence
	9	19	100.0	19	6	BD137887	BD137887 Detection
	10	19	100.0	19	6	BD188058	BD188058 Method fo
	11	19	100.0	19	6	BD243828	BD243828 Detection
	12	19	100.0	19	6	CQ786443	CQ786443 Sequence
	13	19	100.0	19	6	CQ813043	CQ813043 Sequence
	14	19	100.0	19	6	E30053	E30053 Method for
	15	19	100.0	19	6	E38244	E38244 Oligonucleo
	16	19	100.0	19	6	I12481	I12481 Sequence 1
	17	19	100.0	19	6	I32094	I32094 Sequence 38
	18	19	100.0	19	6	I43102	I43102 Sequence 1
	19	19	100.0	19	6	I44633	I44633 Sequence 1
	20	19	100.0	19	6	I51812	I51812 Sequence 1
	21	19	100.0	19	6	I74346	I74346 Sequence 1
	22	19	100.0	19	6	AR200612	AR200612 Sequence
	23	19	100.0	19	6	AR241366	AR241366 Sequence
	24	19	100.0	19	6	AR256570	AR256570 Sequence
	25	19	100.0	19	6	AR429569	AR429569 Sequence
	26	19	100.0	19	6	AR534210	AR534210 Sequence
	27	19	100.0	19	6	AX016778	AX016778 Sequence
	28	19	100.0	19	6	AX082724	AX082724 Sequence
	29	19	100.0	19	6	AX195369	AX195369 Sequence
	30	19	100.0	19	6	AX375721	AX375721 Sequence
	31	19	100.0	19	6	AX523786	AX523786 Sequence
	32	19	100.0	19	6	AX592667	AX592667 Sequence
	33	19	100.0	19	6	BD003393	BD003393 Methods a
	34	19	100.0	19	6	BD074168	BD074168 Examinati
C	35	19	100.0	20	6	AR159689	AR159689 Sequence
C	36	19	100.0	20	6	I13120	I13120 Sequence 20
C	37	19	100.0	20	6	I33592	I33592 Sequence 14
C	38	19	100.0	20	6	BD016824	BD016824 Copper-to
C	39	19	100.0	20	6	BD101856	BD101856 Copper to
C	40	19	100.0	30	6	A23661	A23661 Yeast 18s r
C	41	19	100.0	30	6	I20028	I20028 Sequence 14
	42	19	100.0	31	8	AB032108s4	AB032111 Geosmithi
	43	19	100.0	31	8	AB032112s4	AB032115 Geosmithi
	44	19	100.0	31	8	AB032116s4	AB032119 Geosmithi
	45	19	100.0	31	8	PC16SRR2	X14982 Pneumocysti

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; Search time 324.949  
Seconds

(without alignments)  
346.132 Million cell

updates/sec

Title: US-10-623-880-1  
Perfect score: 19  
Sequence: 1 tccgtaggtgaacctgcgg 19

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	19	2	AAQ94390	Aaq94390 18S ribos
2	19	100.0	19	2	AAQ91601	Aaq91601 Candida s
3	19	100.0	19	2	AAT84759	Aat84759 Primer IT
4	19	100.0	19	2	AAT75520	Aat75520 Candida u
5	19	100.0	19	2	AAV62538	Aav62538 Ribosomal
6	19	100.0	19	2	AAV59022	Aav59022 Internal

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	7	19	100.0	19	2	AAV43271 Aav43271 PCR prime
	8	19	100.0	19	2	AAV24005 Aav24005 Primer IT
	9	19	100.0	19	2	AAT89973 Aat89973 Candida a
	10	19	100.0	19	2	AAZ09820 Aaz09820 Phytophth
	11	19	100.0	19	2	AAV83709 Aav83709 PCR prime
	12	19	100.0	19	2	AAZ06547 Aaz06547 Oligonuc1
	13	19	100.0	19	3	AAZ60489 Aaz60489 PCR prime
	14	19	100.0	19	3	AAZ91727 Aaz91727 PCR prime
	15	19	100.0	19	3	AAZ24495 Aaz24495 H. capsul
	16	19	100.0	19	3	AAA92483 Aaa92483 Fungal ri
	17	19	100.0	19	3	AAA94771 Aaa94771 PCR prime
	18	19	100.0	19	4	AAF75131 Aaf75131 Fungal pa
	19	19	100.0	19	4	AAC93016 Aac93016 C. cibari
	20	19	100.0	19	4	AAS08395 Aas08395 Internal
	21	19	100.0	19	4	AAC91829 Aac91829 C. cibari
	22	19	100.0	19	4	AAC91161 Aac91161 Universal
	23	19	100.0	19	6	ABS70017 Abs70017 Aspergill
	24	19	100.0	19	6	ABA94546 Aba94546 Mycosphae
	25	19	100.0	19	8	ACC50003 Acc50003 Oligonuc1
	26	19	100.0	19	9	ACC47145 Acc47145 Nucleotid
	27	19	100.0	19	10	ABV77013 Abv77013 Primer IT
	28	19	100.0	19	12	ADH61955 Adh61955 Panellus
	29	19	100.0	19	12	ADK23612 Adk23612 Fungal un
	30	19	100.0	19	12	ADM56196 Adm56196 Myrotheci
	31	19	100.0	19	12	ADN61575 Adn61575 Fungi, oo
C	32	19	100.0	20	2	AAQ71863 Aaq71863 Eucaryoti
C	33	19	100.0	20	2	AAT59959 Aat59959 Primer TW
C	34	19	100.0	20	4	AAS08629 Aas08629 Cordyceps
C	35	19	100.0	20	6	AAI99898 Aai99898 PCR prime
C	36	19	100.0	20	12	ADH43086 Adh43086 NS8 prime
C	37	19	100.0	30	2	AAQ27207 Aaq27207 PDGF-B pr
C	38	19	100.0	30	12	ADP19598 Adp19598 Oligonuc1
	39	19	100.0	82	4	AAH26400 Aah26400 Arabidops
	40	19	100.0	253	4	AAH42943 Aah42943 Nucleic a
	41	19	100.0	253	8	ABX96743 Abx96743 D. melano
	42	19	100.0	272	8	ABZ55168 Abz55168 Aspergill
	43	19	100.0	276	12	ADL16003 Adl16003 white rot
	44	19	100.0	344	5	AAH42541 Aah42541 Nucleotid
	45	19	100.0	345	4	AAH44596 Aah44596 Pneumocysti

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; Search time 96.9487  
Seconds

(without alignments)  
320.677 Million cell

updates/sec

Title: US-10-623-880-1  
Perfect score: 19  
Sequence: 1 tccgtaggtgaacctgcgg 19

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	19	1	US-08-065-845-1	Sequence 1, Appli
2	19	100.0	19	1	US-08-233-608-38	Sequence 38, Appl
3	19	100.0	19	1	US-08-429-523-1	Sequence 1, Appli
4	19	100.0	19	1	US-08-429-532-1	Sequence 1, Appli
5	19	100.0	19	1	US-08-429-522-1	Sequence 1, Appli
6	19	100.0	19	1	US-08-429-520-1	Sequence 1, Appli
7	19	100.0	19	1	US-08-742-023-9	Sequence 9, Appli
8	19	100.0	19	1	US-08-887-480-38	Sequence 38, Appl
9	19	100.0	19	1	US-08-905-314A-1	Sequence 1, Appli
10	19	100.0	19	2	US-08-722-187-38	Sequence 38, Appl
11	19	100.0	19	3	US-08-968-505-9	Sequence 9, Appli
12	19	100.0	19	3	US-09-258-967-1	Sequence 1, Appli
13	19	100.0	19	3	US-09-269-136B-1	Sequence 1, Appli
14	19	100.0	19	3	US-09-635-747-1	Sequence 1, Appli

Untitled						
	15	19	100.0	19	3 US-09-026-601-1	Sequence 1, Appli
	16	19	100.0	19	3 US-09-673-298-1	Sequence 1, Appli
	17	19	100.0	19	4 US-09-481-293-1	Sequence 1, Appli
	18	19	100.0	19	4 US-09-939-379B-1	Sequence 1, Appli
	19	19	100.0	19	4 US-09-961-663-1	Sequence 1, Appli
	20	19	100.0	19	5 PCT-US95-04712-38	Sequence 38, Appl
c	21	19	100.0	20	1 US-08-093-144-20	Sequence 20, Appl
c	22	19	100.0	20	1 US-08-448-204-14	Sequence 14, Appl
c	23	19	100.0	20	3 US-09-450-656-29	Sequence 29, Appl
c	24	19	100.0	30	1 US-08-094-079-14	Sequence 14, Appl
	25	19	100.0	261	4 US-09-248-796A-13393	Sequence 13393, A
	26	19	100.0	344	3 US-09-488-295-1	Sequence 1, Appli
	27	19	100.0	353	2 US-08-722-187-84	Sequence 84, Appl
	28	19	100.0	353	5 PCT-US95-04712-84	Sequence 84, Appl
	29	19	100.0	370	3 US-09-450-656-2	Sequence 2, Appli
	30	19	100.0	515	4 US-09-517-790-1	Sequence 1, Appli
	31	19	100.0	523	4 US-09-517-790-4	Sequence 4, Appli
	32	19	100.0	534	1 US-08-233-608-5	Sequence 5, Appli
	33	19	100.0	534	1 US-08-887-480-5	Sequence 5, Appli
	34	19	100.0	534	2 US-08-722-187-5	Sequence 5, Appli
	35	19	100.0	534	4 US-09-961-663-17	Sequence 17, Appl
	36	19	100.0	534	5 PCT-US95-04712-5	Sequence 5, Appli
	37	19	100.0	535	1 US-08-742-023-1	Sequence 1, Appli
	38	19	100.0	535	3 US-08-968-505-1	Sequence 1, Appli
	39	19	100.0	536	1 US-08-742-023-2	Sequence 2, Appli
	40	19	100.0	536	3 US-08-968-505-2	Sequence 2, Appli
	41	19	100.0	536	4 US-09-517-790-5	Sequence 5, Appli
	42	19	100.0	540	1 US-08-233-608-6	Sequence 6, Appli
	43	19	100.0	540	1 US-08-887-480-6	Sequence 6, Appli
	44	19	100.0	540	2 US-08-722-187-6	Sequence 6, Appli
	45	19	100.0	540	4 US-09-961-663-18	Sequence 18, Appl

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; search time 2777.9  
Seconds

(without alignments)  
45.570 Million cell

updates/sec

Title: US-10-623-880-1  
Perfect score: 19  
Sequence: 1 tccgtaggtgaacctgcgg 19

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 7389322 seqs, 3331285599 residues

Word size : 0

Total number of hits satisfying chosen parameters: 14778644

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:\*  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*  
22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:\*  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

Untitled  
SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	19	9	US-09-961-663-1	Sequence 1, Appli
2	19	100.0	19	10	US-09-939-379B-1	Sequence 1, Appli
3	19	100.0	19	10	US-09-961-755A-9	Sequence 9, Appli
4	19	100.0	19	14	US-10-199-559-1	Sequence 1, Appli
5	19	100.0	19	17	US-10-623-880-1	Sequence 1, Appli
6	19	100.0	19	19	US-10-468-250A-145	Sequence 145, App
7	19	100.0	19	20	US-10-773-904-9	Sequence 9, Appli
8	19	100.0	19	20	US-10-773-905-9	Sequence 9, Appli
9	19	100.0	19	22	US-10-757-093-24	Sequence 24, Appl
10	19	100.0	19	22	US-10-514-861-31	Sequence 31, Appl
c 11	19	100.0	20	15	US-10-252-093-2	Sequence 2, Appli
12	19	100.0	80	14	US-10-216-540-25	Sequence 25, Appl
13	19	100.0	253	9	US-09-768-020-59	Sequence 59, Appl
14	19	100.0	345	18	US-10-009-980B-7	Sequence 7, Appli
c 15	19	100.0	359	19	US-10-437-963-89865	Sequence 89865, A
c 16	19	100.0	489	13	US-10-027-632-235007	Sequence 235007,
c 17	19	100.0	489	13	US-10-027-632-235008	Sequence 235008,
c 18	19	100.0	489	13	US-10-027-632-235009	Sequence 235009,
c 19	19	100.0	489	17	US-10-027-632-235007	Sequence 235007,
c 20	19	100.0	489	17	US-10-027-632-235008	Sequence 235008,
c 21	19	100.0	489	17	US-10-027-632-235009	Sequence 235009,
c 22	19	100.0	507	13	US-10-027-632-218865	Sequence 218865,
c 23	19	100.0	507	17	US-10-027-632-218865	Sequence 218865,
24	19	100.0	534	9	US-09-961-663-17	Sequence 17, Appl
25	19	100.0	540	9	US-09-961-663-18	Sequence 18, Appl
26	19	100.0	616	19	US-10-767-701-5087	Sequence 5087, Ap
27	19	100.0	618	9	US-09-766-173C-5	Sequence 5, Appli
28	19	100.0	641	9	US-09-766-173C-4	Sequence 4, Appli
c 29	19	100.0	870	9	US-09-897-231-4	Sequence 4, Appli
c 30	19	100.0	874	9	US-09-897-231-2	Sequence 2, Appli
c 31	19	100.0	875	9	US-09-897-231-1	Sequence 1, Appli
c 32	19	100.0	875	9	US-09-897-231-3	Sequence 3, Appli
c 33	19	100.0	875	9	US-09-897-231-5	Sequence 5, Appli
c 34	19	100.0	875	9	US-09-897-231-7	Sequence 7, Appli
c 35	19	100.0	876	9	US-09-897-231-6	Sequence 6, Appli
36	19	100.0	1071	18	US-10-424-599-117869	Sequence 117869,
37	19	100.0	1193	9	US-09-897-231-27	Sequence 27, Appl
38	19	100.0	1235	19	US-10-437-963-59964	Sequence 59964, A
c 39	19	100.0	1638	20	US-10-425-115-46831	Sequence 46831, A
40	19	100.0	1798	17	US-10-182-329-110	Sequence 110, App
41	19	100.0	1798	18	US-10-182-327-195	Sequence 195, App
42	19	100.0	1798	19	US-10-361-002-8	Sequence 8, Appli
43	19	100.0	1798	19	US-10-361-004-8	Sequence 8, Appli
44	19	100.0	1869	17	US-10-182-329-111	Sequence 111, App
45	19	100.0	1869	17	US-10-182-329-112	Sequence 112, App



OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; Search time 2543.08

Seconds

(without alignments)

284.388 Million cell

updates/sec

Title: US-10-623-880-1

Perfect score: 19

Sequence: 1 tccgtaggtgaacctgcgg 19

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_htc:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	50	1	AU104891	AU104891 AU104891
2	19	100.0	70	1	AI083317	AI083317 SWAMCAC19
3	19	100.0	72	7	W91795	W91795 SWAMCA1047S
4	19	100.0	73	2	AW600150	AW600150 SWL4CAK10
5	19	100.0	73	2	AW600166	AW600166 SWL4CAK10
6	19	100.0	90	1	AA842703	AA842703 MBAFCZ9E1
c 7	19	100.0	91	9	AL943905	AL943905 Arabidops
8	19	100.0	94	2	AW140194	AW140194 SWAMCAC44
9	19	100.0	99	2	AW600205	AW600205 SWL4CAK11
10	19	100.0	99	7	CF356199	CF356199 maj52e05.
c 11	19	100.0	106	2	BE699876	BE699876 MRO-NN008

Untitled

c	12	19	100.0	107	8	BH428817	BH428817	BOHPD80TR
c	13	19	100.0	109	5	BW443181	BW443181	BW443181
	14	19	100.0	113	1	AI066826	AI066826	SWAMCAC19
c	15	19	100.0	115	5	BW442554	BW442554	BW442554
	16	19	100.0	116	2	BE758448	BE758448	SWYACAL10
c	17	19	100.0	117	8	BH526719	BH526719	BOHSC35TF
	18	19	100.0	118	1	AA232008	AA232008	SWMFCA131
c	19	19	100.0	119	5	BW227691	BW227691	BW227691
	20	19	100.0	122	6	CB884448	CB884448	Ma0003 Ha
c	21	19	100.0	124	8	BH443909	BH443909	BOGHN51TF
	22	19	100.0	126	1	AA661396	AA661396	MBAFCW3E0
	23	19	100.0	127	6	CD374809	CD374809	TNWbmfC9E
	24	19	100.0	129	8	BZ520871	BZ520871	BOMRW03TR
	25	19	100.0	130	8	BZ463311	BZ463311	BOOAR51TF
	26	19	100.0	139	2	BE758507	BE758507	SWYACAL11
	27	19	100.0	142	4	BJ396485	BJ396485	BJ396485
	28	19	100.0	143	1	AA509105	AA509105	MBAFCX7D0
c	29	19	100.0	143	5	BW446696	BW446696	BW446696
	30	19	100.0	144	1	AA056801	AA056801	SWMFCA101
	31	19	100.0	144	2	BE132429	BE132429	SWYACAL09
	32	19	100.0	144	7	N43357	N43357	SWMFCA372SK
c	33	19	100.0	144	9	AG230502	AG230502	Lotus cor
c	34	19	100.0	145	7	CF890788	CF890788	UI-CF-EC1
c	35	19	100.0	146	6	CB518218	CB518218	VCXR-1-01
c	36	19	100.0	147	5	BW445099	BW445099	BW445099
	37	19	100.0	148	2	AW172168	AW172168	SWL4CAK07
c	38	19	100.0	150	7	CV356796	CV356796	MR4-RT004
	39	19	100.0	151	1	AA990946	AA990946	BSBmMFSZ0
	40	19	100.0	151	2	BE758465	BE758465	SWYACAL11
	41	19	100.0	153	8	CC325309	CC325309	XM149 Bay
	42	19	100.0	155	1	AA180660	AA180660	MBAFCG2D0
	43	19	100.0	155	8	CC178106	CC178106	XE271 Bay
c	44	19	100.0	157	7	CV243517	CV243517	WS0252.B2
	45	19	100.0	160	2	AW680221	AW680221	WS1_50_H0

OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; search time 1025.64  
Seconds

(without alignments)  
944.877 Million cell

updates/sec

Title: US-10-623-880-27  
Perfect score: 20  
Sequence: 1 ccgggaggggatttctctt 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	6	AR429595	AR429595 Sequence
2	20	100.0	20	6	AX592693	AX592693 Sequence
c 3	20	100.0	460	8	AF065849	AF065849 Venturia
4	17	85.0	177402	2	AC128077	AC128077 Rattus no
5	17	85.0	236563	2	AC131138	AC131138 Rattus no
c 6	16	80.0	458	8	AF065850	AF065850 Cladospor

# Untitled

C	7	16	80.0	460	8	AF065848	AF065848	Venturia
C	8	16	80.0	460	8	AF065851	AF065851	Cladospor
C	9	16	80.0	461	8	AF065836	AF065836	Venturia
C	10	16	80.0	461	8	AF065837	AF065837	Venturia
C	11	16	80.0	461	8	AF065845	AF065845	Venturia
C	12	16	80.0	461	8	AF065846	AF065846	Venturia
C	13	16	80.0	461	8	AF333447	AF333447	Venturia
C	14	16	80.0	461	8	AF333448	AF333448	Venturia
C	15	16	80.0	461	8	AF333449	AF333449	Venturia
C	16	16	80.0	461	8	AF333450	AF333450	Venturia
C	17	16	80.0	462	8	AF065838	AF065838	Venturia
C	18	16	80.0	462	8	AF065839	AF065839	Venturia
C	19	16	80.0	462	8	AF065840	AF065840	Venturia
C	20	16	80.0	462	8	AF065841	AF065841	Venturia
C	21	16	80.0	462	8	AF065842	AF065842	Venturia
C	22	16	80.0	462	8	AF333440	AF333440	Venturia
C	23	16	80.0	462	8	AF333441	AF333441	Venturia
C	24	16	80.0	462	8	AF333442	AF333442	Venturia
C	25	16	80.0	462	8	AF333443	AF333443	Venturia
C	26	16	80.0	462	8	AF333444	AF333444	Venturia
C	27	16	80.0	462	8	AF333445	AF333445	Venturia
C	28	16	80.0	462	8	AF333446	AF333446	Venturia
C	29	16	80.0	462	8	AF338402	AF338402	Spilocaea
C	30	16	80.0	463	8	AF065843	AF065843	Venturia
C	31	16	80.0	463	8	AF065844	AF065844	Venturia
C	32	16	80.0	463	8	AF065847	AF065847	Venturia
C	33	16	80.0	463	8	AF338399	AF338399	Spilocaea
C	34	16	80.0	463	8	AF338400	AF338400	Spilocaea
C	35	16	80.0	463	8	AF338401	AF338401	Spilocaea
C	36	16	80.0	491	8	AY251085	AY251085	Fusicladi
C	37	16	80.0	492	8	AY251084	AY251084	Fusicladi
C	38	16	80.0	501	8	AY173018	AY173018	Venturia
C	39	16	80.0	501	8	AY177406	AY177406	Venturia
C	40	16	80.0	515	8	AY251082	AY251082	Fusicladi
C	41	16	80.0	518	8	AY251083	AY251083	Pseudocla
C	42	16	80.0	522	8	AF531078	AF531078	Venturia
C	43	16	80.0	532	8	AF333438	AF333438	Venturia
C	44	16	80.0	541	8	AY361999	AY361999	Fusicladi
C	45	16	80.0	541	8	AF393685	AF393685	Fusicladi

OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; Search time 342.051  
Seconds

(without alignments)  
346.132 Million cell

updates/sec

Title: US-10-623-880-27  
Perfect score: 20  
Sequence: 1 ccgggcgagggatttctctt 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	
	1	20	100.0	20	10	ABV77037	Abv77037 Primer Vc
c	2	16	80.0	600	10	ADG37681	Adg37681 Aspergill
c	3	16	80.0	1662	5	AAH65558	Aah65558 C glutami
	4	16	80.0	3602	10	ADB69027	Adb69027 C. neofor
	5	16	80.0	349980	5	AAH68525	Aah68525 C glutami
	6	15	75.0	510	6	ABQ26634	Abq26634 oligonuc1
c	7	15	75.0	510	6	ABQ26635	Abq26635 oligonuc1

# Untitled

c	8	15	75.0	1176	8	ACA32188	Aca32188 Prokaryot
c	9	15	75.0	1400	3	AAZ49433	Aaz49433 E.coli K
	10	15	75.0	1468	6	ABQ48562	Abq48562 Oligonuc1
c	11	15	75.0	1468	6	ABQ48563	Abq48563 Oligonuc1
c	12	15	75.0	22130	6	ABS78850	Abs78850 E. coli C
c	13	15	75.0	22130	10	ADH80417	Adh80417 Escherich
c	14	15	75.0	26173	9	ACD19056	Acd19056 E. coli 0
c	15	15	75.0	38155	9	ACD19066	Acd19066 E. coli 0
	16	15	75.0	44029	10	ADC00710	Adc00710 Enterohae
	17	15	75.0	45175	9	ACD19103	Acd19103 E.coli 0
c	18	15	75.0	48423	10	ADC00439	Adc00439 Enterohae
c	19	15	75.0	49650	10	ADC00365	Adc00365 Enterohae
c	20	15	75.0	49795	9	ACD19047	Acd19047 E.coli 0
c	21	15	75.0	58175	10	ADC00292	Adc00292 Enterohae
	22	15	75.0	91740	10	ADC00956	Adc00956 Enterohae
c	23	15	75.0	110000	12	ADN46845_01	Continuation (2 of
	24	15	75.0	110000	12	ADN47591_18	Continuation (19 o
	25	15	75.0	110000	12	ADN47591_19	Continuation (20 o
c	26	15	75.0	110000	12	ADN46123_01	Continuation (2 of
	27	15	75.0	110000	12	ADN47209_18	Continuation (19 o
	28	15	75.0	110000	12	ADN47209_19	Continuation (20 o
c	29	15	75.0	110000	12	ADN46464_01	Continuation (2 of
	30	15	75.0	110000	12	ADN47960_18	Continuation (19 o
	31	15	75.0	110000	12	ADN47960_19	Continuation (20 o
c	32	15	75.0	134141	6	ABN83487	Abn83487 Escherich
	33	14	70.0	232	4	AAF79990	Aaf79990 Nucleotid
c	34	14	70.0	289	2	AAV88814	Aav88814 EST clone
c	35	14	70.0	300	2	AAZ14988	Aaz14988 Human gen
	36	14	70.0	303	5	AAS86933	Aas86933 DNA encod
	37	14	70.0	405	4	AAF83395	Aaf83395 P. chryso
	38	14	70.0	405	4	AAF83396	Aaf83396 P. chryso
c	39	14	70.0	451	9	ACH27903	Ach27903 Human adu
c	40	14	70.0	558	13	ADQ78945	Adq78945 Novel can
	41	14	70.0	643	8	ABX63812	Abx63812 Human cDN
c	42	14	70.0	649	13	ACN54120	Acn54120 Cotton an
c	43	14	70.0	726	8	ACF39401	Acf39401 Mycobacte
c	44	14	70.0	831	4	AAH06449	Aah06449 Human cDN
	45	14	70.0	834	11	ACN92285	Acn92285 Breast ca

OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; Search time 102.051  
Seconds

(without alignments)  
320.677 Million cell

updates/sec

Title: US-10-623-880-27  
Perfect score: 20  
Sequence: 1 ccgggcgagggatttctctt 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	4	US-09-939-379B-27	Sequence 27, Appl
c 2	15	75.0	26173	3	US-09-453-702B-69	Sequence 69, Appl
c 3	15	75.0	38155	3	US-09-453-702B-79	Sequence 79, Appl
4	15	75.0	45175	3	US-09-453-702B-116	Sequence 116, App
c 5	15	75.0	49795	3	US-09-453-702B-60	Sequence 60, Appl
6	14	70.0	1281	4	US-09-902-540-7744	Sequence 7744, Ap
c 7	14	70.0	1309	2	US-08-933-750C-63	Sequence 63, Appl
c 8	14	70.0	1309	3	US-09-234-613-63	Sequence 63, Appl
c 9	14	70.0	2513	4	US-09-016-434-1166	Sequence 1166, Ap
c 10	14	70.0	2513	4	US-09-949-016-904	Sequence 904, App
c 11	14	70.0	2521	4	US-09-949-016-1755	Sequence 1755, Ap
c 12	14	70.0	5641	4	US-09-902-540-767	Sequence 767, App
c 13	14	70.0	12453	4	US-09-949-016-12646	Sequence 12646, A
c 14	14	70.0	12460	4	US-09-949-016-13497	Sequence 13497, A

Untitled							
	15	14	70.0	16442	3	US-08-781-891-208	Sequence 208, App
	16	14	70.0	16442	4	US-09-618-166-208	Sequence 208, App
c	17	14	70.0	28136	4	US-09-949-016-16317	Sequence 16317, A
	18	14	70.0	52971	4	US-09-949-016-16452	Sequence 16452, A
	19	14	70.0	89716	4	US-09-949-016-11900	Sequence 11900, A
c	20	14	70.0	670689	4	US-09-949-016-12505	Sequence 12505, A
c	21	14	70.0	670690	4	US-09-949-016-14207	Sequence 14207, A
c	22	14	70.0	784019	4	US-09-949-016-14033	Sequence 14033, A
c	23	14	70.0	828152	4	US-09-949-016-12777	Sequence 12777, A
	24	14	70.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	25	14	70.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	26	13	65.0	16	4	US-09-939-379B-25	Sequence 25, Appl
c	27	13	65.0	219	3	US-09-056-556-218	Sequence 218, App
c	28	13	65.0	219	3	US-09-072-596-213	Sequence 213, App
c	29	13	65.0	219	4	US-09-072-967-218	Sequence 218, App
	30	13	65.0	243	4	US-09-252-991A-4273	Sequence 4273, Ap
	31	13	65.0	352	2	US-08-692-511-1	Sequence 1, Appli
c	32	13	65.0	355	3	US-09-328-111-558	Sequence 558, App
c	33	13	65.0	522	1	US-07-778-156-4	Sequence 4, Appli
c	34	13	65.0	522	2	US-08-422-166-4	Sequence 4, Appli
c	35	13	65.0	563	3	US-09-385-982-434	Sequence 434, App
	36	13	65.0	601	4	US-09-949-016-79117	Sequence 79117, A
	37	13	65.0	601	4	US-09-949-016-79118	Sequence 79118, A
	38	13	65.0	601	4	US-09-949-016-79119	Sequence 79119, A
	39	13	65.0	601	4	US-09-949-016-79120	Sequence 79120, A
c	40	13	65.0	601	4	US-09-949-016-83352	Sequence 83352, A
c	41	13	65.0	601	4	US-09-949-016-107767	Sequence 107767,
c	42	13	65.0	601	4	US-09-949-016-107768	Sequence 107768,
	43	13	65.0	601	4	US-09-949-016-165565	Sequence 165565,
c	44	13	65.0	601	4	US-09-949-016-206916	Sequence 206916,
	45	13	65.0	610	3	US-09-385-982-229	Sequence 229, App



OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; search time 2924.1  
Seconds

(without alignments)  
45.570 Million cell

updates/sec

Title: US-10-623-880-27  
Perfect score: 20  
Sequence: 1 ccgggaggggatttctctt 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 7389322 seqs, 333128559 residues

Word size : 0

Total number of hits satisfying chosen parameters: 14778644

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

Untitled  
SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	10	US-09-939-379B-27	Sequence 27, Appl
2	20	100.0	20	14	US-10-199-559-27	Sequence 27, Appl
3	20	100.0	20	17	US-10-623-880-27	Sequence 27, Appl
c 4	16	80.0	1662	9	US-09-738-626-593	Sequence 593, App
5	16	80.0	3602	17	US-10-320-797-154	Sequence 154, App
6	16	80.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
7	15	75.0	136	19	US-10-437-963-38131	Sequence 38131, A
8	15	75.0	453	15	US-10-156-761-1914	Sequence 1914, Ap
9	15	75.0	510	20	US-10-363-345A-13225	Sequence 13225, A
c 10	15	75.0	510	20	US-10-363-345A-13226	Sequence 13226, A
11	15	75.0	510	21	US-10-363-483A-13225	Sequence 13225, A
c 12	15	75.0	510	21	US-10-363-483A-13226	Sequence 13226, A
c 13	15	75.0	619	20	US-10-425-115-134035	Sequence 134035,
c 14	15	75.0	1176	17	US-10-282-122A-20058	Sequence 20058, A
15	15	75.0	1292	18	US-10-425-114-18323	Sequence 18323, A
16	15	75.0	1389	20	US-10-425-115-149422	Sequence 149422,
17	15	75.0	1468	20	US-10-363-345A-35153	Sequence 35153, A
c 18	15	75.0	1468	20	US-10-363-345A-35154	Sequence 35154, A
19	15	75.0	1468	21	US-10-363-483A-35153	Sequence 35153, A
c 20	15	75.0	1468	21	US-10-363-483A-35154	Sequence 35154, A
c 21	15	75.0	22130	16	US-10-085-959-17	Sequence 17, Appl
c 22	15	75.0	26173	14	US-10-114-170-69	Sequence 69, Appl
c 23	15	75.0	38155	14	US-10-114-170-79	Sequence 79, Appl
24	15	75.0	45175	14	US-10-114-170-116	Sequence 116, App
c 25	15	75.0	49795	14	US-10-114-170-60	Sequence 60, Appl
c 26	15	75.0	72480	17	US-10-418-837-2	Sequence 2, Appli
c 27	15	75.0	9025608	15	US-10-156-761-1	Sequence 1, Appli
c 28	14	70.0	25	21	US-10-719-900-467742	Sequence 467742,
c 29	14	70.0	25	21	US-10-719-900-972064	Sequence 972064,
30	14	70.0	25	22	US-10-719-956-214222	Sequence 214222,
c 31	14	70.0	25	22	US-10-719-956-692586	Sequence 692586,
32	14	70.0	232	14	US-10-070-676-24	Sequence 24, Appl
c 33	14	70.0	289	13	US-10-040-739-1292	Sequence 1292, Ap
34	14	70.0	303	22	US-10-450-763-22737	Sequence 22737, A
c 35	14	70.0	451	10	US-09-918-995-15115	Sequence 15115, A
36	14	70.0	471	20	US-10-425-115-92035	Sequence 92035, A
c 37	14	70.0	600	22	US-10-972-079-86660	Sequence 86660, A
38	14	70.0	643	13	US-10-044-090-812	Sequence 812, App
c 39	14	70.0	649	19	US-10-021-323-8901	Sequence 8901, Ap
c 40	14	70.0	810	13	US-10-027-632-7665	Sequence 7665, Ap
c 41	14	70.0	810	17	US-10-027-632-7665	Sequence 7665, Ap
c 42	14	70.0	811	13	US-10-027-632-166429	Sequence 166429,
c 43	14	70.0	811	13	US-10-027-632-166430	Sequence 166430,
c 44	14	70.0	811	13	US-10-027-632-166431	Sequence 166431,
c 45	14	70.0	811	13	US-10-027-632-166432	Sequence 166432,

OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; search time 2924.1  
Seconds

(without alignments)  
45.570 Million cell

updates/sec

Title: US-10-623-880-27  
Perfect score: 20  
Sequence: 1 ccgggaggggatttctctt 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 7389322 seqs, 333128559 residues

Word size : 0

Total number of hits satisfying chosen parameters: 14778644

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

Untitled  
SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	10	US-09-939-379B-27	Sequence 27, Appl
2	20	100.0	20	14	US-10-199-559-27	Sequence 27, Appl
3	20	100.0	20	17	US-10-623-880-27	Sequence 27, Appl
c 4	16	80.0	1662	9	US-09-738-626-593	Sequence 593, App
5	16	80.0	3602	17	US-10-320-797-154	Sequence 154, App
6	16	80.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
7	15	75.0	136	19	US-10-437-963-38131	Sequence 38131, A
8	15	75.0	453	15	US-10-156-761-1914	Sequence 1914, Ap
9	15	75.0	510	20	US-10-363-345A-13225	Sequence 13225, A
c 10	15	75.0	510	20	US-10-363-345A-13226	Sequence 13226, A
11	15	75.0	510	21	US-10-363-483A-13225	Sequence 13225, A
c 12	15	75.0	510	21	US-10-363-483A-13226	Sequence 13226, A
c 13	15	75.0	619	20	US-10-425-115-134035	Sequence 134035,
c 14	15	75.0	1176	17	US-10-282-122A-20058	Sequence 20058, A
15	15	75.0	1292	18	US-10-425-114-18323	Sequence 18323, A
16	15	75.0	1389	20	US-10-425-115-149422	Sequence 149422,
17	15	75.0	1468	20	US-10-363-345A-35153	Sequence 35153, A
c 18	15	75.0	1468	20	US-10-363-345A-35154	Sequence 35154, A
19	15	75.0	1468	21	US-10-363-483A-35153	Sequence 35153, A
c 20	15	75.0	1468	21	US-10-363-483A-35154	Sequence 35154, A
c 21	15	75.0	22130	16	US-10-085-959-17	Sequence 17, Appl
c 22	15	75.0	26173	14	US-10-114-170-69	Sequence 69, Appl
c 23	15	75.0	38155	14	US-10-114-170-79	Sequence 79, Appl
24	15	75.0	45175	14	US-10-114-170-116	Sequence 116, App
c 25	15	75.0	49795	14	US-10-114-170-60	Sequence 60, Appl
c 26	15	75.0	72480	17	US-10-418-837-2	Sequence 2, Appli
c 27	15	75.0	9025608	15	US-10-156-761-1	Sequence 1, Appli
c 28	14	70.0	25	21	US-10-719-900-467742	Sequence 467742,
c 29	14	70.0	25	21	US-10-719-900-972064	Sequence 972064,
30	14	70.0	25	22	US-10-719-956-214222	Sequence 214222,
c 31	14	70.0	25	22	US-10-719-956-692586	Sequence 692586,
32	14	70.0	232	14	US-10-070-676-24	Sequence 24, Appl
c 33	14	70.0	289	13	US-10-040-739-1292	Sequence 1292, Ap
34	14	70.0	303	22	US-10-450-763-22737	Sequence 22737, A
c 35	14	70.0	451	10	US-09-918-995-15115	Sequence 15115, A
36	14	70.0	471	20	US-10-425-115-92035	Sequence 92035, A
c 37	14	70.0	600	22	US-10-972-079-86660	Sequence 86660, A
38	14	70.0	643	13	US-10-044-090-812	Sequence 812, App
c 39	14	70.0	649	19	US-10-021-323-8901	Sequence 8901, Ap
c 40	14	70.0	810	13	US-10-027-632-7665	Sequence 7665, Ap
c 41	14	70.0	810	17	US-10-027-632-7665	Sequence 7665, Ap
c 42	14	70.0	811	13	US-10-027-632-166429	Sequence 166429,
c 43	14	70.0	811	13	US-10-027-632-166430	Sequence 166430,
c 44	14	70.0	811	13	US-10-027-632-166431	Sequence 166431,
c 45	14	70.0	811	13	US-10-027-632-166432	Sequence 166432,

# Untitled

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; Search time 2676.92  
Seconds

(without alignments)  
284.388 Million cell

updates/sec

Title: US-10-623-880-27  
Perfect score: 20  
Sequence: 1 ccgggcgagggatttctctt 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	85.0	431	6	CD785534	CD785534 EST656895
2	17	85.0	466	2	BF856215	BF856215 CM4-FN019
3	17	85.0	792	6	CD786033	CD786033 EST657394
4	17	85.0	893	6	CD794511	CD794511 EST665872
c 5	16	80.0	467	7	CK179037	CK179037 EST768357
c 6	16	80.0	479	9	CG679733	CG679733 ZMMBBb031
7	16	80.0	521	7	CK437458	CK437458 GQ0041.BR
8	16	80.0	527	7	CO473798	CO473798 GQ0045.B3
9	16	80.0	532	8	AZ069108	AZ069108 RPCI-23-4
c 10	16	80.0	544	5	BU362724	BU362724 603787416

# Untitled

	11	16	80.0	546	7	CO474354	CO474354	GQ0045.B3
c	12	16	80.0	556	9	CG913575	CG913575	ZMMBBb037
	13	16	80.0	573	7	CK179036	CK179036	EST768356
	14	16	80.0	710	9	AG300383	AG300383	Mus muscu
	15	16	80.0	711	4	BG569377	BG569377	602588695
	16	16	80.0	724	5	BU000509	BU000509	QGG25A09.
c	17	16	80.0	752	9	CG795593	CG795593	ZMMBBb032
	18	16	80.0	791	9	CG689000	CG689000	ZMMBBc012
	19	16	80.0	827	9	CG180063	CG180063	PUIFS71TD
c	20	16	80.0	862	9	CNS03ARJ	AL235576	Tetraodon
c	21	16	80.0	867	7	CN833033	CN833033	AGENCOURT
	22	16	80.0	928	9	CG077859	CG077859	PUJDF38TB
c	23	16	80.0	948	8	BZ081313	BZ081313	1kf87d06.
	24	16	80.0	1003	9	CL199390	CL199390	ZMMBBc007
c	25	16	80.0	1153	9	AG128376	AG128376	Pan trogl
c	26	15	75.0	112	4	BM516383	BM516383	kj69e02.y
c	27	15	75.0	273	7	CF327617	CF327617	NACL--02-
	28	15	75.0	305	8	AZ577615	AZ577615	11h09 sho
	29	15	75.0	340	1	AA807740	AA807740	nw27c12.s
c	30	15	75.0	420	1	AJ480572	AJ480572	AJ480572
c	31	15	75.0	439	9	CG998755	CG998755	ZMMBBb053
c	32	15	75.0	454	2	BE367271	BE367271	PI1_44_E0
c	33	15	75.0	458	4	BG355454	BG355454	EM1_16_F0
	34	15	75.0	466	2	AW340130	AW340130	hc93f12.x
c	35	15	75.0	477	4	BM319936	BM319936	ki80f05.y
	36	15	75.0	477	7	CK149415	CK149415	1742OTEX5
c	37	15	75.0	485	5	BU979426	BU979426	HA16C02r
c	38	15	75.0	491	4	BG280699	BG280699	c5g08np.r
c	39	15	75.0	499	2	BE455006	BE455006	HVSMEh009
c	40	15	75.0	499	4	BM374819	BM374819	EBma05_SQ
c	41	15	75.0	533	7	CK149461	CK149461	1742OTEX6
c	42	15	75.0	552	5	BU979447	BU979447	HA16D03r
	43	15	75.0	600	7	CF753483	CF753483	EST-Conti
c	44	15	75.0	607	5	BU983985	BU983985	HA31K06r
	45	15	75.0	613	9	CL912826	CL912826	OA_Aba001

OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 13:04:33 ; Search time 1819 Seconds  
(without alignments)  
506.129 Million cell

updates/sec

Title: US-10-623-880-1  
Perfect score: 19  
Sequence: 1 tccgtaggtgaacctgcgg 19

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 578008

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	19	6	AR036914	AR036914 Sequence
2	19	100.0	19	6	AR043154	AR043154 Sequence
3	19	100.0	19	6	AR050515	AR050515 Sequence
4	19	100.0	19	6	AR074654	AR074654 Sequence
5	19	100.0	19	6	AR097249	AR097249 Sequence
6	19	100.0	19	6	AR147481	AR147481 Sequence
7	19	100.0	19	6	AR153773	AR153773 Sequence

# Untitled

8	19	100.0	19	6	AR178320	AR178320 Sequence
9	19	100.0	19	6	BD137887	BD137887 Detection
10	19	100.0	19	6	BD188058	BD188058 Method fo
11	19	100.0	19	6	BD243828	BD243828 Detection
12	19	100.0	19	6	CQ786443	CQ786443 Sequence
13	19	100.0	19	6	CQ813043	CQ813043 Sequence
14	19	100.0	19	6	E30053	E30053 Method for
15	19	100.0	19	6	E38244	E38244 Oligonucleo
16	19	100.0	19	6	I12481	I12481 Sequence 1
17	19	100.0	19	6	I32094	I32094 Sequence 38
18	19	100.0	19	6	I43102	I43102 Sequence 1
19	19	100.0	19	6	I44633	I44633 Sequence 1
20	19	100.0	19	6	I51812	I51812 Sequence 1
21	19	100.0	19	6	I74346	I74346 Sequence 1
22	19	100.0	19	6	AR200612	AR200612 Sequence
23	19	100.0	19	6	AR241366	AR241366 Sequence
24	19	100.0	19	6	AR256570	AR256570 Sequence
25	19	100.0	19	6	AR429569	AR429569 Sequence
26	19	100.0	19	6	AR534210	AR534210 Sequence
27	19	100.0	19	6	AX016778	AX016778 Sequence
28	19	100.0	19	6	AX082724	AX082724 Sequence
29	19	100.0	19	6	AX195369	AX195369 Sequence
30	19	100.0	19	6	AX375721	AX375721 Sequence
31	19	100.0	19	6	AX523786	AX523786 Sequence
32	19	100.0	19	6	AX592667	AX592667 Sequence
33	19	100.0	19	6	BD003393	BD003393 Methods a
34	19	100.0	19	6	BD074168	BD074168 Examinati
C 35	17	89.5	19	6	CQ868753	CQ868753 Sequence
C 36	16	84.2	17	6	AR186637	AR186637 Sequence
C 37	16	84.2	17	6	AR186638	AR186638 Sequence
C 38	16	84.2	17	6	AR323268	AR323268 Sequence
C 39	16	84.2	17	6	AR323269	AR323269 Sequence
40	16	84.2	19	6	CQ830761	CQ830761 Sequence
C 41	15	78.9	17	6	AR327596	AR327596 Sequence
42	15	78.9	18	6	CQ848503	CQ848503 Sequence
43	13	68.4	13	6	AR082394	AR082394 Sequence
C 44	13	68.4	17	6	AR327597	AR327597 Sequence
C 45	12	63.2	17	6	AR327595	AR327595 Sequence



OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 12:19:43 ; Search time 417 Seconds  
(without alignments)  
269.724 Million cell

updates/sec

Title: US-10-623-880-1  
Perfect score: 19  
Sequence: 1 tccgtaggtgaacctgcgg 19

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1679476

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	19	2	AAQ94390	Aaq94390 18S ribos
2	19	100.0	19	2	AAQ91601	Aaq91601 Candida s
3	19	100.0	19	2	AAT84759	Aat84759 Primer IT
4	19	100.0	19	2	AAT75520	Aat75520 Candida u
5	19	100.0	19	2	AAV62538	Aav62538 Ribosomal
6	19	100.0	19	2	AAV59022	Aav59022 Internal
7	19	100.0	19	2	AAV43271	Aav43271 PCR prime
8	19	100.0	19	2	AAV24005	Aav24005 Primer IT

Untitled

	9	19	100.0	19	2	AAT89973	Aat89973	Candida a
	10	19	100.0	19	2	AAZ09820	Aaz09820	Phytophth
	11	19	100.0	19	2	AAV83709	Aav83709	PCR prime
	12	19	100.0	19	2	AAZ06547	Aaz06547	oligonucl
	13	19	100.0	19	3	AAZ60489	Aaz60489	PCR prime
	14	19	100.0	19	3	AAZ91727	Aaz91727	PCR prime
	15	19	100.0	19	3	AAZ24495	Aaz24495	H. capsul
	16	19	100.0	19	3	AAA92483	Aaa92483	Fungal ri
	17	19	100.0	19	3	AAA94771	Aaa94771	PCR prime
	18	19	100.0	19	4	AAF75131	Aaf75131	Fungal pa
	19	19	100.0	19	4	AAC93016	Aac93016	C. cibari
	20	19	100.0	19	4	AAS08395	Aas08395	Internal
	21	19	100.0	19	4	AAC91829	Aac91829	C. cibari
	22	19	100.0	19	4	AAC91161	Aac91161	Universal
	23	19	100.0	19	6	ABS70017	Abs70017	Aspergill
	24	19	100.0	19	6	ABA94546	Aba94546	Mycosphae
	25	19	100.0	19	8	ACC50003	Acc50003	oligonucl
	26	19	100.0	19	9	ACC47145	Acc47145	Nucleotid
	27	19	100.0	19	10	ABV77013	Abv77013	Primer IT
	28	19	100.0	19	12	ADH61955	Adh61955	Panelus
	29	19	100.0	19	12	ADK23612	Adk23612	Fungal un
	30	19	100.0	19	12	ADM56196	Adm56196	Myrotheci
	31	19	100.0	19	12	ADN61575	Adn61575	Fungi, oo
c	32	18	94.7	18	12	ADJ57011	Adj57011	Primer 18
	33	18	94.7	19	4	AAH03087	Aah03087	Microorga
	34	18	94.7	19	9	ADA27511	Ada27511	Micoorgan
c	35	17	89.5	19	13	ADR69344	Adr69344	Novel mol
c	36	16	84.2	16	2	AAQ50414	Aaq50414	Primer 2
c	37	16	84.2	16	2	AAT02856	Aat02856	Fungus-de
c	38	16	84.2	17	2	AAX69376	Aax69376	Human flt
c	39	16	84.2	17	2	AAX69375	Aax69375	Human flt
c	40	16	84.2	19	10	ADF35943	Adf35943	Human VEG
	41	16	84.2	19	10	ADF36370	Adf36370	Human VEG
c	42	14	73.7	18	2	AAV54103	Aav54103	Nucleotid
c	43	14	73.7	18	2	AAV60124	Aav60124	PCR prime
c	44	14	73.7	18	2	AAV61685	Aav61685	Fusarium
	45	13	68.4	13	2	AAV09940	Aav09940	Nucleotid

Untitled  
GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 14:43:20 ; Search time 124 Seconds  
(without alignments)  
250.720 Million cell

updates/sec

Title: US-10-623-880-1  
Perfect score: 19  
Sequence: 1 tccgtaggtgaacctgcgg 19

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 276054

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	19	100.0	19	1	US-08-065-845-1
2	19	100.0	19	1	US-08-233-608-38
3	19	100.0	19	1	US-08-429-523-1
4	19	100.0	19	1	US-08-429-532-1
5	19	100.0	19	1	US-08-429-522-1
6	19	100.0	19	1	US-08-429-520-1
7	19	100.0	19	1	US-08-742-023-9
8	19	100.0	19	1	US-08-887-480-38
9	19	100.0	19	1	US-08-905-314A-1
10	19	100.0	19	2	US-08-722-187-38
11	19	100.0	19	3	US-08-968-505-9
12	19	100.0	19	3	US-09-258-967-1
13	19	100.0	19	3	US-09-269-136B-1
14	19	100.0	19	3	US-09-635-747-1
15	19	100.0	19	3	US-09-026-601-1

				Untitled		
	16	19	100.0	19 3	US-09-673-298-1	Sequence 1, Appli
	17	19	100.0	19 4	US-09-481-293-1	Sequence 1, Appli
	18	19	100.0	19 4	US-09-939-379B-1	Sequence 1, Appli
	19	19	100.0	19 4	US-09-961-663-1	Sequence 1, Appli
	20	19	100.0	19 5	PCT-US95-04712-38	Sequence 38, Appl
	21	18	94.7	19 3	US-09-311-260-111	Sequence 111, App
c	22	16	84.2	17 3	US-08-584-040-2125	Sequence 2125, Ap
c	23	16	84.2	17 3	US-08-584-040-2126	Sequence 2126, Ap
c	24	16	84.2	17 4	US-09-371-772B-670	Sequence 670, App
c	25	16	84.2	17 4	US-09-371-772B-671	Sequence 671, App
c	26	16	84.2	17 4	US-09-685-664B-670	Sequence 670, App
c	27	16	84.2	17 4	US-09-685-664B-671	Sequence 671, App
c	28	15	78.9	17 4	US-09-371-772B-4998	Sequence 4998, Ap
	29	13	68.4	13 2	US-08-883-920-6	Sequence 6, Appli
c	30	13	68.4	17 4	US-09-371-772B-4999	Sequence 4999, Ap
c	31	12	63.2	17 4	US-09-371-772B-4997	Sequence 4997, Ap
c	32	12	63.2	17 4	US-09-371-772B-5000	Sequence 5000, Ap
	33	12	63.2	18 4	US-09-856-662-74	Sequence 74, Appl
	34	12	63.2	19 1	US-08-796-883-13	Sequence 13, Appl
	35	12	63.2	19 2	US-08-531-864-13	Sequence 13, Appl
	36	12	63.2	19 2	US-08-373-636C-13	Sequence 13, Appl
	37	12	63.2	19 3	US-08-602-506A-13	Sequence 13, Appl
	38	12	63.2	19 3	US-09-266-294-13	Sequence 13, Appl
	39	12	63.2	19 3	US-09-179-281-13	Sequence 13, Appl
	40	12	63.2	19 4	US-09-747-391-1	Sequence 1, Appli
	41	12	63.2	19 4	US-09-747-391-119	Sequence 119, App
c	42	11	57.9	16 4	US-09-371-772B-5911	Sequence 5911, Ap
c	43	11	57.9	17 3	US-08-584-040-2127	Sequence 2127, Ap
c	44	11	57.9	17 4	US-09-371-772B-672	Sequence 672, App
c	45	11	57.9	17 4	US-09-685-664B-672	Sequence 672, App

OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 14:39:49 ; Search time 605 Seconds  
(without alignments)  
209.238 Million cell

updates/sec

Title: US-10-623-880-1  
Perfect score: 19  
Sequence: 1 tccgtaggtgaacctgcgg 19

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 7389322 seqs, 3331285599 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1397872

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# Untitled

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	19	9	US-09-961-663-1	Sequence 1, Appli
2	19	100.0	19	10	US-09-939-379B-1	Sequence 1, Appli
3	19	100.0	19	10	US-09-961-755A-9	Sequence 9, Appli
4	19	100.0	19	14	US-10-199-559-1	Sequence 1, Appli
5	19	100.0	19	17	US-10-623-880-1	Sequence 1, Appli
6	19	100.0	19	19	US-10-468-250A-145	Sequence 145, App
7	19	100.0	19	20	US-10-773-904-9	Sequence 9, Appli
8	19	100.0	19	20	US-10-773-905-9	Sequence 9, Appli
9	19	100.0	19	22	US-10-757-093-24	Sequence 24, Appl
10	19	100.0	19	22	US-10-514-861-31	Sequence 31, Appl
11	18	94.7	19	10	US-09-802-110B-111	Sequence 111, App
c 12	16	84.2	17	18	US-10-138-674-670	Sequence 670, App
c 13	16	84.2	17	18	US-10-138-674-671	Sequence 671, App
c 14	16	84.2	17	19	US-10-287-949A-670	Sequence 670, App
c 15	16	84.2	17	19	US-10-287-949A-671	Sequence 671, App
c 16	16	84.2	19	19	US-10-665-951-232	Sequence 232, App
17	16	84.2	19	19	US-10-665-951-659	Sequence 659, App
c 18	16	84.2	19	21	US-10-758-155-232	Sequence 232, App
19	16	84.2	19	21	US-10-758-155-659	Sequence 659, App
c 20	16	84.2	19	22	US-10-831-620-232	Sequence 232, App
21	16	84.2	19	22	US-10-831-620-659	Sequence 659, App
c 22	16	84.2	19	22	US-10-844-076-232	Sequence 232, App
23	16	84.2	19	22	US-10-844-076-659	Sequence 659, App
c 24	15	78.9	17	18	US-10-138-674-4998	Sequence 4998, Ap
c 25	15	78.9	17	19	US-10-287-949A-4998	Sequence 4998, Ap
c 26	15	78.9	17	20	US-10-712-633-935	Sequence 935, App
c 27	14	73.7	17	18	US-10-138-674-7830	Sequence 7830, Ap
c 28	14	73.7	17	19	US-10-287-949A-7830	Sequence 7830, Ap
c 29	14	73.7	17	20	US-10-712-633-934	Sequence 934, App
c 30	13	68.4	17	18	US-10-138-674-4999	Sequence 4999, Ap
c 31	13	68.4	17	19	US-10-287-949A-4999	Sequence 4999, Ap
c 32	12	63.2	17	18	US-10-138-674-4997	Sequence 4997, Ap
c 33	12	63.2	17	18	US-10-138-674-5000	Sequence 5000, Ap
c 34	12	63.2	17	19	US-10-287-949A-4997	Sequence 4997, Ap
c 35	12	63.2	17	19	US-10-287-949A-5000	Sequence 5000, Ap
c 36	12	63.2	18	9	US-09-875-338-88	Sequence 88, Appl
c 37	12	63.2	18	14	US-10-077-023-88	Sequence 88, Appl
38	12	63.2	18	21	US-10-920-184-74	Sequence 74, Appl
39	12	63.2	19	16	US-10-133-779-1	Sequence 1, Appli
40	12	63.2	19	16	US-10-133-779-119	Sequence 119, App
c 41	11	57.9	16	18	US-10-138-674-5911	Sequence 5911, Ap
c 42	11	57.9	16	19	US-10-287-949A-5911	Sequence 5911, Ap
c 43	11	57.9	17	18	US-10-138-674-672	Sequence 672, App
c 44	11	57.9	17	19	US-10-287-949A-672	Sequence 672, App
c 45	11	57.9	17	20	US-10-712-633-936	Sequence 936, App

OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 12:53:08 ; Search time 3022 Seconds  
(without alignments)  
239.319 Million cell

updates/sec

Title: US-10-623-880-1  
Perfect score: 19  
Sequence: 1 tccgtaggtgaacctgcgg 19

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9364

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	9	47.4	10	9	CL438130	CL438130 PST6863-N
C 2	8	42.1	19	2	AW246513	AW246513 2821739.3
3	8	42.1	19	8	AZ644418	AZ644418 1M0508B20
4	8	42.1	19	8	AZ835621	AZ835621 2M0129L21
C 5	7	36.8	13	9	AJ587972	AJ587972 Arabidops
C 6	7	36.8	15	6	CA851407	CA851407 D13D09_G0
C 7	7	36.8	16	9	CL423510	CL423510 O1S0557-0
C 8	7	36.8	17	1	AJ654055	AJ654055 AJ654055
C 9	7	36.8	18	9	AJ594669	AJ594669 Arabidops
C 10	7	36.8	19	7	CO791279	CO791279 NT012A_A0
C 11	7	36.8	19	8	AZ331326	AZ331326 1M0059B15
C 12	7	36.8	19	8	AZ345449	AZ345449 1M0080I08

# Untitled

c	13	7	36.8	19	8	AZ345511	AZ345511	1M0080J01
c	14	7	36.8	19	8	AZ345536	AZ345536	1M0080O06
c	15	7	36.8	19	8	AZ345572	AZ345572	1M0080J17
c	16	7	36.8	19	8	AZ346709	AZ346709	1M0082M06
c	17	7	36.8	19	8	AZ346710	AZ346710	1M0082N01
c	18	7	36.8	19	8	AZ368837	AZ368837	1M0119A11
c	19	7	36.8	19	8	AZ447223	AZ447223	1M0244H13
c	20	7	36.8	19	8	AZ447247	AZ447247	1M0244G19
	21	7	36.8	19	8	AZ477382	AZ477382	1M0296P16
c	22	7	36.8	19	8	AZ482658	AZ482658	1M0307L16
	23	7	36.8	19	8	AZ500335	AZ500335	1M0338G07
c	24	7	36.8	19	8	AZ510096	AZ510096	1M0354B22
c	25	7	36.8	19	8	AZ510106	AZ510106	1M0354E19
c	26	7	36.8	19	8	AZ634762	AZ634762	1M0490C18
c	27	7	36.8	19	8	AZ638980	AZ638980	1M0499L08
	28	7	36.8	19	8	AZ651870	AZ651870	1M0522M15
	29	7	36.8	19	8	AZ655467	AZ655467	1M0530O17
c	30	7	36.8	19	8	AZ827164	AZ827164	2M0103M22
c	31	6	31.6	10	9	AJ598893	AJ598893	Arabidops
c	32	6	31.6	10	9	CL437066	CL437066	PST4433-N
c	33	6	31.6	11	1	AJ663404	AJ663404	AJ663404
c	34	6	31.6	11	4	BG927896	BG927896	HNC45-1-D
	35	6	31.6	11	5	BQ592717	BQ592717	E012124-0
c	36	6	31.6	11	5	BQ595402	BQ595402	E012693-0
	37	6	31.6	11	9	CL437175	CL437175	PST4640-N
	38	6	31.6	12	1	AJ747414	AJ747414	AJ747414
	39	6	31.6	12	1	AJ747580	AJ747580	AJ747580
	40	6	31.6	13	1	AJ679030	AJ679030	AJ679030
	41	6	31.6	13	8	BH170808	BH170808	SALK_0033
	42	6	31.6	13	9	AJ588255	AJ588255	Arabidops
	43	6	31.6	13	9	AJ594173	AJ594173	Arabidops
	44	6	31.6	13	9	AJ598721	AJ598721	Arabidops
c	45	6	31.6	14	1	AJ655566	AJ655566	AJ655566



Untitled  
GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 15:40:55 ; Search time 1830 seconds  
(without alignments)  
529.565 Million cell

updates/sec

Title: US-10-623-880-27  
Perfect score: 20  
Sequence: 1 ccgggcgagggatttctctt 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 790860

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	6	AR429595	AR429595 Sequence
2	20	100.0	20	6	AX592693	AX592693 Sequence
3	13	65.0	16	6	AR429593	AR429593 Sequence
4	13	65.0	16	6	AX592691	AX592691 Sequence
c 5	12	60.0	20	6	AR116448	AR116448 Sequence
c 6	12	60.0	20	6	AX020008	AX020008 Sequence
c 7	12	60.0	20	6	BD074605	BD074605 Antisense

# Untitled

C	8	11	55.0	17	6	AR192354	AR192354	Sequence
C	9	11	55.0	17	6	AR326223	AR326223	Sequence
C	10	11	55.0	17	6	AX757656	AX757656	Sequence
C	11	11	55.0	19	6	AX298780	AX298780	Sequence
	12	11	55.0	20	6	AX111309	AX111309	Sequence
C	13	11	55.0	20	6	AX474051	AX474051	Sequence
	14	10	50.0	11	6	AR301743	AR301743	Sequence
C	15	10	50.0	11	6	AX623235	AX623235	Sequence
C	16	10	50.0	11	6	AX630656	AX630656	Sequence
	17	10	50.0	11	6	BD124493	BD124493	Compositi
C	18	10	50.0	17	6	AR186718	AR186718	Sequence
C	19	10	50.0	17	6	AR323349	AR323349	Sequence
	20	10	50.0	17	6	AX214909	AX214909	Sequence
	21	10	50.0	17	6	AX214910	AX214910	Sequence
	22	10	50.0	17	6	AX214911	AX214911	Sequence
	23	10	50.0	17	6	AX214912	AX214912	Sequence
	24	10	50.0	17	6	AX215791	AX215791	Sequence
	25	10	50.0	17	6	AX216769	AX216769	Sequence
	26	10	50.0	17	6	AX217116	AX217116	Sequence
C	27	10	50.0	17	6	AX756835	AX756835	Sequence
C	28	10	50.0	17	6	AX761071	AX761071	Sequence
	29	10	50.0	18	6	AR175669	AR175669	Sequence
	30	10	50.0	18	6	BD224873	BD224873	Antisense
	31	10	50.0	18	6	AR195245	AR195245	Sequence
	32	10	50.0	18	6	AR211095	AR211095	Sequence
	33	10	50.0	18	6	AR222327	AR222327	Sequence
	34	10	50.0	18	6	AR241446	AR241446	Sequence
C	35	10	50.0	18	6	AR298065	AR298065	Sequence
	36	10	50.0	18	6	AX705641	AX705641	Sequence
C	37	10	50.0	18	6	AX705643	AX705643	Sequence
	38	10	50.0	18	6	AX822833	AX822833	Sequence
	39	10	50.0	18	6	AX826473	AX826473	Sequence
	40	10	50.0	18	6	BD014812	BD014812	Modulator
	41	10	50.0	20	4	DOGP34901	L24236 Dog (Clone:	
	42	10	50.0	20	6	AR092413	AR092413	Sequence
	43	10	50.0	20	6	AR116535	AR116535	Sequence
C	44	10	50.0	20	6	AR233669	AR233669	Sequence
	45	10	50.0	20	6	AR293020	AR293020	Sequence

OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 14:50:20 ; Search time 415 Seconds  
(without alignments)  
285.289 Million cell

updates/sec

Title: US-10-623-880-27  
Perfect score: 20  
Sequence: 1 ccgggcgagggatttctctt 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2207178

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description	
1	20	100.0	20	10	ABV77037	Abv77037 Primer Vc
2	13	65.0	16	10	ABV77035	Abv77035 Primer Vc
c 3	12	60.0	20	2	AAZ00572	Aaz00572 Human GPC
c 4	12	60.0	20	2	AAX29329	Aax29329 JNK2-spec
c 5	12	60.0	20	3	AAC62872	Aac62872 JNK antis
c 6	12	60.0	20	8	ADA26576	Ada26576 Human Jun
7	12	60.0	20	10	ADC55474	Adc55474 Primer #3
c 8	12	60.0	20	12	ADN48318	Adn48318 Human Jun

# Untitled

	9	11	55.0	13	5	ABC59176	Abc59176	Oligonuc1
C	10	11	55.0	13	5	ABC59175	Abc59175	Oligonuc1
	11	11	55.0	13	5	ABC59174	Abc59174	Oligonuc1
C	12	11	55.0	13	5	ABC59177	Abc59177	Oligonuc1
C	13	11	55.0	17	2	AAX75092	Aax75092	Mouse flt
C	14	11	55.0	17	2	AAV95270	Aav95270	Human c-f
C	15	11	55.0	17	10	ADB40654	Adb40654	Tumour su
	16	11	55.0	18	2	AAV51658	Aav51658	Zea mays
C	17	11	55.0	19	6	AAS97804	Aas97804	Murine SA
C	18	11	55.0	19	12	ADM16144	Adm16144	Murine SA
	19	11	55.0	20	4	AAH02049	Aah02049	gyrA resi
C	20	11	55.0	20	6	ABN89794	Abn89794	Human ABC
	21	10	50.0	10	3	AAZ84641	Aaz84641	Metastati
	22	10	50.0	10	6	ABL01198	Ab101198	Human AKR
	23	10	50.0	11	2	AAZ19014	Aaz19014	Murine MR
C	24	10	50.0	11	6	ABV62490	Abv62490	Human ski
C	25	10	50.0	11	6	ABV69911	Abv69911	Human ski
C	26	10	50.0	13	5	ABF30081	Abf30081	Oligonuc1
	27	10	50.0	13	5	ABF30080	Abf30080	Oligonuc1
	28	10	50.0	15	4	AAF45167	Aaf45167	IGFBP2 ol
	29	10	50.0	15	4	AAF45166	Aaf45166	IGFBP2 ol
	30	10	50.0	15	4	AAF45162	Aaf45162	IGFBP2 ol
	31	10	50.0	15	4	AAF45163	Aaf45163	IGFBP2 ol
	32	10	50.0	15	4	AAF45164	Aaf45164	IGFBP2 ol
	33	10	50.0	15	4	AAF45165	Aaf45165	IGFBP2 ol
	34	10	50.0	15	6	ABL01152	Ab101152	Human AKR
C	35	10	50.0	17	2	AAX69456	Aax69456	Human flt
	36	10	50.0	17	4	ABK01233	Abk01233	Human NOG
	37	10	50.0	17	4	ABK00353	Abk00353	Human NOG
	38	10	50.0	17	4	ABK02558	Abk02558	Human NOG
	39	10	50.0	17	4	ABK00352	Abk00352	Human NOG
	40	10	50.0	17	4	ABK02211	Abk02211	Human NOG
	41	10	50.0	17	4	ABK00351	Abk00351	Human NOG
	42	10	50.0	17	4	ABK00354	Abk00354	Human NOG
C	43	10	50.0	17	10	ADB44069	Adb44069	Tumour su
C	44	10	50.0	17	10	ADB39833	Adb39833	Tumour su
	45	10	50.0	18	2	AAT16422	Aat16422	Primer #1

OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 16:21:40 ; Search time 123 Seconds  
(without alignments)  
266.061 Million cell

updates/sec

Title: US-10-623-880-27  
Perfect score: 20  
Sequence: 1 ccgggcgagggatttctctt 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 401682

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	20	100.0	20	4	US-09-939-379B-27
2	13	65.0	16	4	US-09-939-379B-25
c 3	12	60.0	20	2	US-08-910-629A-29
c 4	12	60.0	20	3	US-09-287-796-29
c 5	12	60.0	20	3	US-09-130-616-29
c 6	12	60.0	20	4	US-09-774-809-29
c 7	11	55.0	17	3	US-08-998-099-10
c 8	11	55.0	17	3	US-08-584-040-7842
c 9	11	55.0	17	4	US-09-371-772B-3625
c 10	11	55.0	17	4	US-09-685-664B-3625
11	10	50.0	11	4	US-09-249-155A-324
c 12	10	50.0	17	3	US-08-584-040-2206
c 13	10	50.0	17	4	US-09-371-772B-751
c 14	10	50.0	17	4	US-09-685-664B-751
15	10	50.0	18	3	US-08-485-942A-69

Untitled						
	16	10	50.0	18	3 US-08-488-214A-69	Sequence 69, Appl
	17	10	50.0	18	3 US-08-488-208A-69	Sequence 69, Appl
	18	10	50.0	18	3 US-09-723-534-22	Sequence 22, Appl
	19	10	50.0	18	3 US-08-483-211A-69	Sequence 69, Appl
	20	10	50.0	18	3 US-08-488-223A-69	Sequence 69, Appl
	21	10	50.0	18	3 US-09-167-109-8	Sequence 8, Appli
	22	10	50.0	18	3 US-08-438-431A-69	Sequence 69, Appl
	23	10	50.0	18	4 US-08-488-225A-69	Sequence 69, Appl
c	24	10	50.0	18	4 US-09-422-978-9800	Sequence 9800, Ap
	25	10	50.0	20	2 US-09-289-368-84	Sequence 84, Appl
	26	10	50.0	20	3 US-09-287-796-116	Sequence 116, App
	27	10	50.0	20	3 US-09-130-616-116	Sequence 116, App
c	28	10	50.0	20	3 US-09-360-416-31	Sequence 31, Appl
	29	10	50.0	20	4 US-09-422-978-4755	Sequence 4755, Ap
c	30	10	50.0	20	4 US-09-198-452A-2980	Sequence 2980, Ap
c	31	10	50.0	20	4 US-09-198-452A-5733	Sequence 5733, Ap
c	32	10	50.0	20	4 US-09-780-172-68	Sequence 68, Appl
	33	10	50.0	20	4 US-09-774-809-116	Sequence 116, App
	34	9	45.0	10	3 US-08-482-073-16	Sequence 16, Appl
c	35	9	45.0	12	2 US-08-173-489C-340	Sequence 340, App
	36	9	45.0	12	3 US-09-281-418-125	Sequence 125, App
c	37	9	45.0	12	4 US-09-497-855A-50	Sequence 50, Appl
c	38	9	45.0	15	2 US-08-765-176-1	Sequence 1, Appli
c	39	9	45.0	15	2 US-08-585-684B-2085	Sequence 2085, Ap
c	40	9	45.0	15	3 US-09-038-073-2085	Sequence 2085, Ap
	41	9	45.0	15	3 US-09-081-646-202	Sequence 202, App
	42	9	45.0	15	3 US-09-081-646-743	Sequence 743, App
c	43	9	45.0	15	3 US-09-423-233-40	Sequence 40, Appl
c	44	9	45.0	16	1 US-08-233-030-52	Sequence 52, Appl
	45	9	45.0	16	4 US-09-371-772B-5653	Sequence 5653, Ap

OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 16:23:55 ; Search time 602 Seconds  
(without alignments)  
221.348 Million cell

updates/sec

Title: US-10-623-880-27  
Perfect score: 20  
Sequence: 1 ccgggcgagggatttctctt 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 7389322 seqs, 3331285599 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1761270

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

Untitled

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	10	US-09-939-379B-27	Sequence 27, Appl
2	20	100.0	20	14	US-10-199-559-27	Sequence 27, Appl
3	20	100.0	20	17	US-10-623-880-27	Sequence 27, Appl
4	13	65.0	16	10	US-09-939-379B-25	Sequence 25, Appl
5	13	65.0	16	14	US-10-199-559-25	Sequence 25, Appl
6	13	65.0	16	17	US-10-623-880-25	Sequence 25, Appl
c 7	12	60.0	20	10	US-09-774-809-29	Sequence 29, Appl
c 8	12	60.0	20	17	US-10-345-444B-29	Sequence 29, Appl
9	11	55.0	13	20	US-10-257-017B-59191	Sequence 59191, A
c 10	11	55.0	13	20	US-10-257-017B-59192	Sequence 59192, A
11	11	55.0	13	20	US-10-257-017B-59193	Sequence 59193, A
c 12	11	55.0	13	20	US-10-257-017B-59194	Sequence 59194, A
c 13	11	55.0	17	18	US-10-138-674-3625	Sequence 3625, Ap
c 14	11	55.0	17	19	US-10-287-949A-3625	Sequence 3625, Ap
c 15	11	55.0	19	18	US-10-280-183A-414	Sequence 414, App
c 16	11	55.0	20	14	US-10-005-338B-205	Sequence 205, App
17	11	55.0	20	20	US-10-767-441-11	Sequence 11, Appl
18	10	50.0	11	17	US-10-314-322-324	Sequence 324, App
19	10	50.0	13	20	US-10-257-017B-130077	Sequence 130077,
c 20	10	50.0	13	20	US-10-257-017B-130078	Sequence 130078,
21	10	50.0	17	10	US-09-780-533A-351	Sequence 351, App
22	10	50.0	17	10	US-09-780-533A-352	Sequence 352, App
23	10	50.0	17	10	US-09-780-533A-353	Sequence 353, App
24	10	50.0	17	10	US-09-780-533A-354	Sequence 354, App
25	10	50.0	17	10	US-09-780-533A-1233	Sequence 1233, Ap
26	10	50.0	17	10	US-09-780-533A-2211	Sequence 2211, Ap
27	10	50.0	17	10	US-09-780-533A-2558	Sequence 2558, Ap
c 28	10	50.0	17	18	US-10-138-674-751	Sequence 751, App
c 29	10	50.0	17	18	US-10-138-674-7881	Sequence 7881, Ap
c 30	10	50.0	17	19	US-10-287-949A-751	Sequence 751, App
c 31	10	50.0	17	19	US-10-287-949A-7881	Sequence 7881, Ap
c 32	10	50.0	17	20	US-10-712-633-1013	Sequence 1013, Ap
33	10	50.0	18	9	US-09-736-084-69	Sequence 69, Appl
34	10	50.0	18	14	US-10-067-125-8	Sequence 8, Appli
c 35	10	50.0	18	17	US-10-349-143-9800	Sequence 9800, Ap
36	10	50.0	18	20	US-10-730-488-69	Sequence 69, Appl
37	10	50.0	18	21	US-10-486-319A-310	Sequence 310, App
c 38	10	50.0	18	21	US-10-486-319A-312	Sequence 312, App
c 39	10	50.0	19	19	US-10-665-951-251	Sequence 251, App
40	10	50.0	19	19	US-10-665-951-678	Sequence 678, App
41	10	50.0	19	21	US-10-920-608-15	Sequence 15, Appl
c 42	10	50.0	19	21	US-10-758-155-251	Sequence 251, App
43	10	50.0	19	21	US-10-758-155-678	Sequence 678, App
44	10	50.0	19	21	US-10-652-791-6	Sequence 6, Appli
c 45	10	50.0	19	21	US-10-652-791-95	Sequence 95, Appl



Untitled  
GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 16:11:25 ; Search time 3007 Seconds  
(without alignments)  
253.171 Million cell

updates/sec

Title: US-10-623-880-27  
Perfect score: 20  
Sequence: 1 ccgggcgcagggatttctctt 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12452

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	9	45.0	15	7	CF303956	CF303956 ABF1--03-
2	9	45.0	19	7	C0783722	C0783722 BL018D_B0
3	9	45.0	20	7	CF306120	CF306120 HDA1--02-
4	9	45.0	20	8	AZ339855	AZ339855 1M0071E03
5	8	40.0	10	9	CL437947	CL437947 PST6577-N
6	8	40.0	11	7	CF304450	CF304450 ABF1--05-
c 7	8	40.0	16	5	BQ588093	BQ588093 E012336-0
c 8	8	40.0	18	6	CD530428	CD530428 06D22 Ara
c 9	8	40.0	18	9	AJ587746	AJ587746 Arabidops
10	8	40.0	19	1	AI027323	AI027323 ow46a07.s
11	8	40.0	19	1	AI371092	AI371092 ta07g09.x
12	8	40.0	19	8	AZ345499	AZ345499 1M0080F06

# Untitled

C	13	8	40.0	19	8	AZ418201	AZ418201	1M0194M12
	14	8	40.0	19	8	AZ440413	AZ440413	1M0231A01
	15	8	40.0	19	8	AZ786336	AZ786336	2M0031H17
	16	8	40.0	19	8	AZ839439	AZ839439	2M0135L06
C	17	8	40.0	19	8	AZ874072	AZ874072	2M0188M06
C	18	8	40.0	19	8	AZ954943	AZ954943	2M0220P16
C	19	8	40.0	19	9	CL657902	CL657902	PRI012d_D
	20	8	40.0	20	8	AZ782717	AZ782717	2M0023N21
C	21	8	40.0	20	8	AZ796553	AZ796553	2M0052P15
	22	7	35.0	12	9	AJ593912	AJ593912	Arabidops
	23	7	35.0	12	9	AJ594491	AJ594491	Arabidops
	24	7	35.0	13	1	AJ666341	AJ666341	AJ666341
	25	7	35.0	13	9	AJ590284	AJ590284	Arabidops
	26	7	35.0	13	9	AJ592721	AJ592721	Arabidops
	27	7	35.0	13	9	AJ593606	AJ593606	Arabidops
	28	7	35.0	13	9	AJ593693	AJ593693	Arabidops
	29	7	35.0	13	9	AJ593750	AJ593750	Arabidops
	30	7	35.0	13	9	AJ594409	AJ594409	Arabidops
	31	7	35.0	13	9	AJ594448	AJ594448	Arabidops
C	32	7	35.0	13	9	AJ599821	AJ599821	Arabidops
	33	7	35.0	14	5	BQ593808	BQ593808	E012763-0
	34	7	35.0	14	9	AJ587585	AJ587585	Arabidops
	35	7	35.0	14	9	AJ592722	AJ592722	Arabidops
	36	7	35.0	14	9	AJ592942	AJ592942	Arabidops
	37	7	35.0	15	7	CF304766	CF304766	ABF1--05-
	38	7	35.0	15	9	AJ593961	AJ593961	Arabidops
	39	7	35.0	15	9	AJ595331	AJ595331	Arabidops
	40	7	35.0	16	4	BG926060	BG926060	HNC23-1-E
	41	7	35.0	16	5	BQ588621	BQ588621	E012562-0
	42	7	35.0	16	7	CF323664	CF323664	HDN--04-H
C	43	7	35.0	16	9	CL437728	CL437728	PST6187-N
	44	7	35.0	17	9	AJ587904	AJ587904	Arabidops
	45	7	35.0	18	4	BG927414	BG927414	HNC1-1-H3